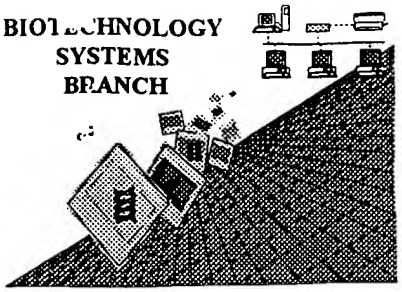

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/847,081

Source: OIPE

Date Processed by STIC: 5/16/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings; thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 09/847,081

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ✓ Wrapped Nucleics — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".

2 ____ Wrapped Aminos — The amino acid number/text at the end of each line "wrapped " down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".

3 ____ Incorrect Line Length — The rules require that a line not exceed 72 characters in length. This includes spaces.

4 ____ Misaligned Amino Acid Numbering — The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 ____ Non-ASCII — This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 ____ Variable Length — Sequence(s) ____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 ____ PatentIn ver. 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

8 ____ Skipped Sequences (OLD RULES) — Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 ____ Skipped Sequences (NEW RULES) — Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ____ Use of **n**'s or **Xaa**'s (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

11 ____ Use of "Artificial" (NEW RULES) — Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

12 ____ Use of <220>Feature (NEW RULES) — Sequence(s) ____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown" **Please explain source of genetic material in <220> to <223> section.** (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 ____ PatentIn ver. 2.0 "bug" — **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING DATE: 05/16/2001
PATENT APPLICATION: US/09/847,081 TIME: 15:06:10

Input Set : A:\DES.txt
Output Set: N:\CRF3\05162001\I847081.raw

Does Not Comply
Corrected Diskette Needed

```
  3 <110> APPLICANT: BAYER AG
  5 <120> TITLE OF INVENTION: DNA encoding the tobacco phytoene synthase
  7 <130> FILE REFERENCE: Le A 34 326
  9 <140> CURRENT APPLICATION NUMBER: US/09/847,081
C--> 10 <141> CURRENT FILING DATE: 2001-05-02
 12 <160> NUMBER OF SEQ ID NOS: 10
 14 <170> SOFTWARE: PatentIn Ver. 2.1
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ERRORED SEQUENCES

```
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 1728
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Nicotiana tabacum
 21 <220> FEATURE:
 22 <221> NAME/KEY: CDS
 23 <222> LOCATION: (244)..(1566)
 25 <400> SEQUENCE: 1
 26 agaaacccag aaagaacaac aggttttgct tcttgttgat gagtgcattt gcctctgctt 60
E--> 28 gtgtaaggca aagtcggttc actttcttat atccgatttt tataatcgtt gaaattagtg
 29 120
E--> 31 gatagactct agtggatatc tacaagtatt ggttttttga taaaataggc tgaggtgaga
 32 180
E--> 34 aggtaacata aaggaaagac aaaaacttgg gaattgtttt agaccaccga ggtttcttgt
 35 240
E--> 37 ttc atg agc atg tct gtt gct ttg ttg tgg gtt gtt tct ccc act tcc
 38 288
 39     Met Ser Met Ser Val Ala Leu Leu Trp Val Val Ser Pro Thr Ser
 40       1               5                  10                  15
E--> 42 gag gtc tcg aat ggg aca gga ttg ttg gat tca gtc cga gaa gga aac
 43 336
 45 Glu Val Ser Asn Gly Thr Gly Leu Leu Asp Ser Val Arg Glu Gly Asn
 46                  20                  25                  30
E--> 48 cgc gtc ttt gta tca tcc agg ttc cta gct cga gat agg aat ttg atg
 49 384
 51 Arg Val Phe Val Ser Ser Arg Phe Leu Ala Arg Asp Arg Asn Leu Met
 52              35                  40                  45
E--> 54 tgg aat ggg aga atc aag aaa ggt ggg aga caa agg tgg aat ttt ggc
 55 432
 57 Trp Asn Gly Arg Ile Lys Lys Gly Gly Arg Gln Arg Trp Asn Phe Gly
 58          50                  55                  60
E--> 60 tct tta att gct gat cca aga tat tca tgc ttg ggt gga tca aga act
 61 480
 64 Ser Leu Ile Ala Asp Pro Arg Tyr Ser Cys Leu Gly Gly Ser Arg Thr
 65      65                  70                  75
E--> 67 gaa aag gga agc act ttc tct gta cag tcc agt ttg gtg gct agc cca
```

Formatera (see item 1 on Error Summary Sheet)

RAW SEQUENCE LISTING DATE: 05/16/2001
PATENT APPLICATION: US/09/847,081 TIME: 15:06:10

Input Set : A:\DES.txt
Output Set: N:\CRF3\05162001\I847081.raw

```
     68 528
     70 Glu Lys Gly Ser Thr Phe Ser Val Gln Ser Ser Leu Val Ala Ser Pro
     71  80                  85                  90                  95
E--> 73 gct gga gaa atg act gtg tca tca gag aaa aag gtg tat gat gtg gta
     74 576
     76 Ala Gly Glu Met Thr Val Ser Ser Glu Lys Lys Val Tyr Asp Val Val
     77                 100                 105                 110
E--> 79 tta aag cag gca gct tta gtg aag agg cag ctg aga tct acc gat gat
     80 624
     82 Leu Lys Gln Ala Ala Leu Val Lys Arg Gln Leu Arg Ser Thr Asp Asp
     83             115                 120                 125
E--> 85 tta gaa gtg aag ccg gat att gtt gtt cca ggg aat ttg ggc ttg ttg
     86 672
     88 Leu Glu Val Lys Pro Asp Ile Val Val Pro Gly Asn Leu Gly Leu Leu
     89         130                 135                 140
E--> 91 agt gaa gca tat gat cgt tgt ggc gaa gta tgt gca gag tat gca aag
     92 720
     94 Ser Glu Ala Tyr Asp Arg Cys Gly Glu Val Cys Ala Glu Tyr Ala Lys
     95     145                 150                 155
E--> 97 aca ttt tac tta gga acc aag cta atg acc cca gag aga aga aga gct
     98 768
    100 Thr Phe Tyr Leu Gly Thr Lys Leu Met Thr Pro Glu Arg Arg Arg Ala
    101 160                 165                 170                 175
E--> 103 atc tgg gca ata tat gtg tgg tgc agg aga acg gat gag ctt gtt gat
    104 816
    106 Ile Trp Ala Ile Tyr Val Trp Cys Arg Arg Thr Asp Glu Leu Val Asp
    107                 180                 185                 190
E--> 109 ggc cct aat gca tcc cac ata act ccg caa gct tta gat agg tgg gag
    110 864
    112 Gly Pro Asn Ala Ser His Ile Thr Pro Gln Ala Leu Asp Arg Trp Glu
    113             195                 200                 205
E--> 115 acc agg ctg gaa gat att ttc agt ggg cgg cca ttt gat atg ctt gat
    116 912
    118 Thr Arg Leu Glu Asp Ile Phe Ser Gly Arg Pro Phe Asp Met Leu Asp
    119         210                 215                 220
E--> 121 gct gct tta tcc gat act gtc tcc aga ttt cct gtt gat att cag cca
    122 960
    124 Ala Ala Leu Ser Asp Thr Val Ser Arg Phe Pro Val Asp Ile Gln Pro
    125     225                 230                 235
E--> 127 ttc aga gat atg att gaa gga atg cgt atg gac ttg tgg aaa tcc aga
    128 1008
    130 Phe Arg Asp Met Ile Glu Gly Met Arg Met Asp Leu Trp Lys Ser Arg
    131 240                 245                 250                 255
E--> 133 tac aaa act ttc gat gag cta tat ctc tat tgt tac tat gtt gct ggt
    134 1056
    136 Tyr Lys Thr Phe Asp Glu Leu Tyr Leu Tyr Cys Tyr Tyr Val Ala Gly
    137                 260                 265                 270
E--> 139 act gta gga ttg atg agt gtt cca gtt atg ggt att gca cct gaa tca
    140 1104
```

RAW SEQUENCE LISTING DATE: 05/16/2001
PATENT APPLICATION: US/09/847,081 TIME: 15:06:10

Input Set : A:\DES.txt
Output Set: N:\CRF3\05162001\I847081.raw

```
     142 Thr Val Gly Leu Met Ser Val Pro Val Met Gly Ile Ala Pro Glu Ser
     143             275                 280                 285
E--> 145 aag gca aca aca gag agt gta tat aat gct gct ttg gct tta ggg ctt
     146 1152
     148 Lys Ala Thr Thr Glu Ser Val Tyr Asn Ala Ala Leu Ala Leu Gly Leu
     149         290                 295                 300
E--> 151 gca aat caa cta acc aat ata ctc aga gat gta gga gaa gat gcc aga
     152 1200
     154 Ala Asn Gln Leu Thr Asn Ile Leu Arg Asp Val Gly Glu Asp Ala Arg
     155     305                 310                 315
E--> 157 aga gga aga gta tac ttg cct caa gat gaa tta gca cag gca ggg ctc
     158 1248
     160 Arg Gly Arg Val Tyr Leu Pro Gln Asp Glu Leu Ala Gln Ala Gly Leu
     161 320                 325                 330                 335
E--> 163 tcc gac gaa gac ata ttt gct gga aga gtg act gat aag tgg agg aac
     164 1296
     166 Ser Asp Glu Asp Ile Phe Ala Gly Arg Val Thr Asp Lys Trp Arg Asn
     167                 340                 345                 350
E--> 169 ttt atg aag aaa caa att cag agg gcg agg aaa ttc ttt gat gag tca
     170 1344
     172 Phe Met Lys Lys Gln Ile Gln Arg Ala Arg Lys Phe Phe Asp Glu Ser
     173             355                 360                 365
E--> 175 gag aaa ggt gtc aca gaa ctg gac tct gct agt aga tgg cct gtg tta
     176 1392
     178 Glu Lys Gly Val Thr Glu Leu Asp Ser Ala Ser Arg Trp Pro Val Leu
     179         370                 375                 380
E--> 181 aca gcg ctg ctg ttg tat cgc aag ata ttg gac gag att gaa gcc aac
     182 1440
     184 Thr Ala Leu Leu Leu Tyr Arg Lys Ile Leu Asp Glu Ile Glu Ala Asn
     185     385                 390                 395
E--> 187 gac tac aac aac ttc aca agg agg gct tat gtt agc aag cca aag aag
     188 1488
     190 Asp Tyr Asn Asn Phe Thr Arg Arg Ala Tyr Val Ser Lys Pro Lys Lys
     191 400                 405                 410                 415
E--> 193 ctt ctc acc ttg ccc att gct tat gca aaa tct ctt gtg ccc cct aat
     194 1536
     196 Leu Leu Thr Leu Pro Ile Ala Tyr Ala Lys Ser Leu Val Pro Pro Asn
     197                 420                 425                 430
E--> 199 aga act tcc tct cca cta gca aag aca tga atgaagtagt tgagtcaatg
     200 1586
     202 Arg Thr Ser Ser Pro Leu Ala Lys Thr
     203             435                 440
E--> 205 agtattatac actaaagaaa ctcaggtact tgtaaatgag atatcttttg ctaaatgtgt
     206 1646
E--> 208 atcatcaaaa gtagattgta aattcaatat gacaatctct tggtagaata ttttctccac
     209 1706
E--> 211 actcatcaaa ccctcaagtg ag
     212 1728
     307 <210> SEQ ID NO: 3
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RAW SEQUENCE LISTING DATE: 05/16/2001
PATENT APPLICATION: US/09/847,081 TIME: 15:06:10

Input Set : A:\DES.txt
Output Set: N:\CRF3\05162001\I847081.raw

```
     308 <211> LENGTH: 1712
     309 <212> TYPE: DNA
     310 <213> ORGANISM: Nicotiana tabacum
     312 <220> FEATURE:
     313 <221> NAME/KEY: CDS
     314 <222> LOCATION: (333)..(1565)
     316 <400> SEQUENCE: 3
W--> 317 cttgaagagt agcagcagca agcaagahaa ttaaagtggg ctatttbkka naagccattg 60
E--> 319 ttacmagara attaagaagc caagamacag gttatttttct acttgagtya ggaaaagttg
     320 120
E--> 322 gtttgcttta tttgtgggct ttttataatc ttttttccac aagggaaagt gggtattttc
     323 180
E--> 325 ttgaaagtgg atttagactc tagtgggaat ctactaggag taaatttatt aatttttttat
     326 240
E--> 328 aaattaagca gaggaaggaa ggaaacagaa aacagaaagt aagacaaaaa accttggaat
     329 300
E--> 331 tgttttagaa agccaaggtt ttcctgttca aa atg tct gtt gcc ttg tta tgg
     332 353
     333                                  Met Ser Val Ala Leu Leu Trp
     334                                    1               5
E--> 336 gtt gtt tca cct tgt gaa gtc tca aat ggg aca gga ttc ttg gat tca
     337 401
     339 Val Val Ser Pro Cys Glu Val Ser Asn Gly Thr Gly Phe Leu Asp Ser
     340          10                  15                  20
E--> 342 gtc cgg gag gga aac cgg gtt ttt gat tcg tcg agg cat agg aat tta
     343 449
     345 Val Arg Glu Gly Asn Arg Val Phe Asp Ser Ser Arg His Arg Asn Leu
     346      25                  30                  35
E--> 348 gtg tgc aat gag aga aac aag aga ggt gtg aaa caa agg tgg aat ttt
     349 497
     351 Val Cys Asn Glu Arg Asn Lys Arg Gly Val Lys Gln Arg Trp Asn Phe
     352  40                  45                  50                  55
E--> 354 ggt tct gta agg tct gct atg gtg gct aca ccg gcg gga gaa atg gcg
     355 545
     357 Gly Ser Val Arg Ser Ala Met Val Ala Thr Pro Ala Gly Glu Met Ala
     358                  60                  65                  70
E--> 360 acg atg aca tca gaa cag atg gtt tat gat gtg gtt tta aaa caa gca
     361 593
     363 Thr Met Thr Ser Glu Gln Met Val Tyr Asp Val Val Leu Lys Gln Ala
     364              75                  80                  85
E--> 366 gct tta gtg aag agg cag ttg aga tct gct gat gat tta gaa gtg aag
     367 641
     369 Ala Leu Val Lys Arg Gln Leu Arg Ser Ala Asp Asp Leu Glu Val Lys
     370          90                  95                 100
E--> 372 ccg gag atc cct ctc ccc ggg aat ttg agc ttg ttg agt gaa gca tat
     373 689
     375 Pro Glu Ile Pro Leu Pro Gly Asn Leu Ser Leu Leu Ser Glu Ala Tyr
     376     105                 110                 115
E--> 378 gat agg tgt agt gaa gta tgt gca gag tat gca aag aca ttt tac tth
```

RAW SEQUENCE LISTING DATE: 05/16/2001
PATENT APPLICATION: US/09/847,081 TIME: 15:06:10

Input Set : A:\DES.txt
Output Set: N:\CRF3\05162001\I847081.raw

```
     379 737
W--> 381 Asp Arg Cys Ser Glu Val Cys Ala Glu Tyr Ala Lys Thr Phe Tyr Xaa
     382 120                 125                 130                 135
E--> 384 gga acc atg yta atg act cca gag aga aga agg gct att tgg gca ata
     385 785
W--> 387 Gly Thr Met Xaa Met Thr Pro Glu Arg Arg Arg Ala Ile Trp Ala Ile
     388                 140                 145                 150
E--> 390 tat gtg tgg tgc agg aga aca gat gaa ctt gtt gat ggc cca aac gca
     391 833
     393 Tyr Val Trp Cys Arg Arg Thr Asp Glu Leu Val Asp Gly Pro Asn Ala
     394             155                 160                 165
E--> 396 tca cat att aca ccc caa gcc tta gat agg tgg gaa gac cgg ctt gaa
     397 881
     399 Ser His Ile Thr Pro Gln Ala Leu Asp Arg Trp Glu Asp Arg Leu Glu
     400         170                 175                 180
E--> 402 gat gtt ttc agc ggg cga cca ttt gat atg ctc gat gct gct ttg tcc
     403 929
     405 Asp Val Phe Ser Gly Arg Pro Phe Asp Met Leu Asp Ala Ala Leu Ser
     406     185                 190                 195
E--> 408 gat act gtt tcc aag ttt cca gtt gat att cag ccg ttc aga gat atg
     409 977
     411 Asp Thr Val Ser Lys Phe Pro Val Asp Ile Gln Pro Phe Arg Asp Met
     412 200                 205                 210                 215
E--> 414 att gaa gga atg cgt atg gac ttg agg aag tca aga tat aga aac ttt
     415 1025
     417 Ile Glu Gly Met Arg Met Asp Leu Arg Lys Ser Arg Tyr Arg Asn Phe
     418                 220                 225                 230
E--> 420 gat gag ctt tac ctc tat tgt tat tac gtt gct ggt acg gtt ggg ttg
     421 1073
     423 Asp Glu Leu Tyr Leu Tyr Cys Tyr Tyr Val Ala Gly Thr Val Gly Leu
     424             235                 240                 245
E--> 426 atg agt gtt cca att atg ggt att gca cct gat tca aag gca aca aca
     427 1121
     429 Met Ser Val Pro Ile Met Gly Ile Ala Pro Asp Ser Lys Ala Thr Thr
     430         250                 255                 260
E--> 432 gag agc gta tat aat gca gct ttg gct tta gga atc gca aat caa cta
     433 1169
     435 Glu Ser Val Tyr Asn Ala Ala Leu Ala Leu Gly Ile Ala Asn Gln Leu
     436     265                 270                 275
E--> 438 acg aac ata ctc aga gat gtt gga gaa gat gcc aga aga gga aga gtc
     439 1217
     441 Thr Asn Ile Leu Arg Asp Val Gly Glu Asp Ala Arg Arg Gly Arg Val
     442 280                 285                 290                 295
E--> 444 tac tta cct caa gat gaa tta gca cag gca ggt ctc ttc gac gat gac
     445 1265
     447 Tyr Leu Pro Gln Asp Glu Leu Ala Gln Ala Gly Leu Phe Asp Asp Asp
     448                 300                 305                 310
E--> 450 ata ttt gct gga aaa gtg act gat aag tgg aga agc ttt atg aag aag
     451 1313
```

RAW SEQUENCE LISTING DATE: 05/16/2001
PATENT APPLICATION: US/09/847,081 TIME: 15:06:10

Input Set : A:\DES.txt
Output Set: N:\CRF3\05162001\I847081.raw

```
     453 Ile Phe Ala Gly Lys Val Thr Asp Lys Trp Arg Ser Phe Met Lys Lys
     454             315                 320                 325
E--> 456 caa atc cag agg gca aga aag ttc ttc gat gag gca gag gaa gga gtt
     457 1361
     459 Gln Ile Gln Arg Ala Arg Lys Phe Phe Asp Glu Ala Glu Glu Gly Val
     460         330                 335                 340
E--> 462 aca caa ctg agc tca gct agc aga tgg cct gta tgg gca tct ttg ctg
     463 1409
     465 Thr Gln Leu Ser Ser Ala Ser Arg Trp Pro Val Trp Ala Ser Leu Leu
     466     345                 350                 355
E--> 468 ttg tac cgc caa ata ctg gac gag att gaa gcc aat gac tac aac aac
     469 1457
     471 Leu Tyr Arg Gln Ile Leu Asp Glu Ile Glu Ala Asn Asp Tyr Asn Asn
     472 360                 365                 370                 375
E--> 474 ttc aca aag aga gct tat gtg agc aaa cca aag aag cta att tcc tta
     475 1505
     477 Phe Thr Lys Arg Ala Tyr Val Ser Lys Pro Lys Lys Leu Ile Ser Leu
     478                 380                 385                 390
E--> 480 cct att gct tat gca aaa tct ctt gtg ccc cct aca aga act ctt gtc
     481 1553
     483 Pro Ile Ala Tyr Ala Lys Ser Leu Val Pro Pro Thr Arg Thr Leu Val
     484             395                 400                 405
E--> 486 acc tct agc taa ggcatagaca tcagatttaa attaaagcaa gaaagcatat
     487 1605
     489 Thr Ser Ser
     490         410
E--> 492 actgttaaaa aagaaagaat ttctaaagta gatattgttg tattgatgcc acttgtatat
     493 1665
E--> 495 catcaaaagt aggtagtaaa atccaatata acaatctcta gtagttg
     496 1712
     499 <210> SEQ ID NO: 4
     500 <211> LENGTH: 410
     501 <212> TYPE: PRT
     502 <213> ORGANISM: Nicotiana tabacum
     504 <400> SEQUENCE: 4
     505 Met Ser Val Ala Leu Leu Trp Val Val Ser Pro Cys Glu Val Ser Asn
     506   1               5                  10                  15
     508 Gly Thr Gly Phe Leu Asp Ser Val Arg Glu Gly Asn Arg Val Phe Asp
     509              20                  25                  30
     511 Ser Ser Arg His Arg Asn Leu Val Cys Asn Glu Arg Asn Lys Arg Gly
     512          35                  40                  45
     514 Val Lys Gln Arg Trp Asn Phe Gly Ser Val Arg Ser Ala Met Val Ala
     515      50                  55                  60
     517 Thr Pro Ala Gly Glu Met Ala Thr Met Thr Ser Glu Gln Met Val Tyr
     518  65                  70                  75                  80
     520 Asp Val Val Leu Lys Gln Ala Ala Leu Val Lys Arg Gln Leu Arg Ser
     521                  85                  90                  95
     523 Ala Asp Asp Leu Glu Val Lys Pro Glu Ile Pro Leu Pro Gly Asn Leu
     524             100                 105                 110
```

RAW SEQUENCE LISTING DATE: 05/16/2001
PATENT APPLICATION: US/09/847,081 TIME: 15:06:10

Input Set : A:\DES.txt
Output Set: N:\CRF3\05162001\I847081.raw

```
     526 Ser Leu Leu Ser Glu Ala Tyr Asp Arg Cys Ser Glu Val Cys Ala Glu
     527         115                 120                 125
E--> 530 Tyr Ala Lys Thr Phe Tyr Xaa Gly Thr Met Xaa Met Thr Pro Glu Arg
     531     130                 135                 140
     533 Arg Arg Ala Ile Trp Ala Ile Tyr Val Trp Cys Arg Arg Thr Asp Glu
     534 145                 150                 155                 160
     536 Leu Val Asp Gly Pro Asn Ala Ser His Ile Thr Pro Gln Ala Leu Asp
     537                 165                 170                 175
     539 Arg Trp Glu Asp Arg Leu Glu Asp Val Phe Ser Gly Arg Pro Phe Asp
     540             180                 185                 190
     542 Met Leu Asp Ala Ala Leu Ser Asp Thr Val Ser Lys Phe Pro Val Asp
     543         195                 200                 205
     545 Ile Gln Pro Phe Arg Asp Met Ile Glu Gly Met Arg Met Asp Leu Arg
     546     210                 215                 220
     548 Lys Ser Arg Tyr Arg Asn Phe Asp Glu Leu Tyr Leu Tyr Cys Tyr Tyr
     549 225                 230                 235                 240
     551 Val Ala Gly Thr Val Gly Leu Met Ser Val Pro Ile Met Gly Ile Ala
     552                 245                 250                 255
     554 Pro Asp Ser Lys Ala Thr Thr Glu Ser Val Tyr Asn Ala Ala Leu Ala
     555             260                 265                 270
     557 Leu Gly Ile Ala Asn Gln Leu Thr Asn Ile Leu Arg Asp Val Gly Glu
     558         275                 280                 285
     560 Asp Ala Arg Arg Gly Arg Val Tyr Leu Pro Gln Asp Glu Leu Ala Gln
     561     290                 295                 300
     563 Ala Gly Leu Phe Asp Asp Asp Ile Phe Ala Gly Lys Val Thr Asp Lys
     564 305                 310                 315                 320
     567 Trp Arg Ser Phe Met Lys Lys Gln Ile Gln Arg Ala Arg Lys Phe Phe
     568                 325                 330                 335
     570 Asp Glu Ala Glu Glu Gly Val Thr Gln Leu Ser Ser Ala Ser Arg Trp
     571             340                 345                 350
     573 Pro Val Trp Ala Ser Leu Leu Leu Tyr Arg Gln Ile Leu Asp Glu Ile
     574         355                 360                 365
     576 Glu Ala Asn Asp Tyr Asn Asn Phe Thr Lys Arg Ala Tyr Val Ser Lys
     577     370                 375                 380
     579 Pro Lys Lys Leu Ile Ser Leu Pro Ile Ala Tyr Ala Lys Ser Leu Val
     580 385                 390                 395                 400
     582 Pro Pro Thr Arg Thr Leu Val Thr Ser Ser
     583                 405                 410
     587 <210> SEQ ID NO: 5
     588 <211> LENGTH: 2205
     589 <212> TYPE: DNA
     590 <213> ORGANISM: Nicotiana tabacum
     592 <220> FEATURE:
     593 <221> NAME/KEY: CDS
     594 <222> LOCATION: (189)..(1955)
     596 <400> SEQUENCE: 5
     597 ctggcatctt acatctgcca aatttctcat ttatagcatc tcctaatctt tagatacctt 60
E--> 599 ttcttcttgt tttgtttttc tatccttcac ttcatgcttt cttgttttac ccatctcttc
     600 120
```

see item 10 on Error Summary Sheet

see item 1 on Error Summary Sheet

RAW SEQUENCE LISTING DATE: 05/16/2001
PATENT APPLICATION: US/09/847,081 TIME: 15:06:10

Input Set : A:\DES.txt
Output Set: N:\CRF3\05162001\I847081.raw

```
E--> 602 cattttcttg gcatttgaca acaaaaggtt ccatttttt tccttttgc tgtatatagc
     603 180
E--> 605 acaattca atg gct act tct tca gct tat ctt tgt tgt cct gca act tct
     606 230
     607          Met Ala Thr Ser Ser Ala Tyr Leu Cys Cys Pro Ala Thr Ser
     608            1               5                  10
E--> 610 gct act gga aag aaa cat att ttg cca aat ggg tca gct gga ttc ttg
     611 278
     612 Ala Thr Gly Lys Lys His Ile Leu Pro Asn Gly Ser Ala Gly Phe Leu
     613  15                  20                  25                  30
E--> 615 gtt ttc cgt ggt ccc cgt ttg tcc aac cgg ttt gtg acc cgg aag tca
     616 326
     617 Val Phe Arg Gly Pro Arg Leu Ser Asn Arg Phe Val Thr Arg Lys Ser
     619                  35                  40                  45
E--> 621 gtt att cgt gct gat ttg gac tcc atg gtc tct gat atg agt act aat
     622 374
     624 Val Ile Arg Ala Asp Leu Asp Ser Met Val Ser Asp Met Ser Thr Asn
     625           50                  55                  60
E--> 627 gct cca aaa ggg cta ttt cca cct gaa cct gaa cat tat cgg ggg cca
     628 422
     630 Ala Pro Lys Gly Leu Phe Pro Pro Glu Pro Glu His Tyr Arg Gly Pro
     631          65                  70                  75
E--> 633 aag ctg aaa gta gct att att gga gct ggg ctt gca ggc atg tca act
     634 470
     636 Lys Leu Lys Val Ala Ile Ile Gly Ala Gly Leu Ala Gly Met Ser Thr
     637      80                  85                  90
E--> 639 gct gtg gag ctc ttg gat caa gga cat gag gtg gat ata tat gaa tca
     640 518
     642 Ala Val Glu Leu Leu Asp Gln Gly His Glu Val Asp Ile Tyr Glu Ser
     643  95                 100                 105                 110
E--> 645 agg cct ttt att ggt ggg aaa gtg gga tct ttt gtt gat aga cgt gga
     646 566
     648 Arg Pro Phe Ile Gly Gly Lys Val Gly Ser Phe Val Asp Arg Arg Gly
     649                 115                 120                 125
E--> 651 aac cac att gaa atg gga ctg cat gtg ttc ttt ggt tgc tat aat aat
     652 614
     654 Asn His Ile Glu Met Gly Leu His Val Phe Phe Gly Cys Tyr Asn Asn
     655             130                 135                 140
E--> 657 ttg ttc cgt ttg tta aaa aag gtg ggt gct gaa aaa aat ctg cta gtg
     658 662
     660 Leu Phe Arg Leu Leu Lys Lys Val Gly Ala Glu Lys Asn Leu Leu Val
     661         145                 150                 155
E--> 663 aag gac cat act cac aca ttt gta aat aaa ggg ggt gaa ata ggg gag
     664 710
     666 Lys Asp His Thr His Thr Phe Val Asn Lys Gly Gly Glu Ile Gly Glu
     667     160                 165                 170
E--> 669 ctt gat ttc cgc ttt cca gtt gga gca ccc cta cac gga att aat gca
     670 758
     672 Leu Asp Phe Arg Phe Pro Val Gly Ala Pro Leu His Gly Ile Asn Ala
```

RAW SEQUENCE LISTING DATE: 05/16/2001
PATENT APPLICATION: US/09/847,081 TIME: 15:06:10

Input Set : A:\DES.txt
Output Set: N:\CRF3\05162001\I847081.raw

```
     673 175                 180                 185                 190
E--> 675 ttt ttg tct acc aat cag cta aag att tat gat aag gct aga aat gct
     676 806
     678 Phe Leu Ser Thr Asn Gln Leu Lys Ile Tyr Asp Lys Ala Arg Asn Ala
     679                 195                 200                 205
E--> 681 gta gct ctt gcc ctt agt cca gtg gtg cgg gct tta gtt gat cca gat
     682 854
     684 Val Ala Leu Ala Leu Ser Pro Val Val Arg Ala Leu Val Asp Pro Asp
     685             210                 215                 220
E--> 687 ggc gcg ttg cag cag ata cgt gat cta gat agt gta agc ttt tca gag
     688 902
     690 Gly Ala Leu Gln Gln Ile Arg Asp Leu Asp Ser Val Ser Phe Ser Glu
     691         225                 230                 235
E--> 693 tgg ttt atg tct aaa ggt ggg acg cgt gct agc atc cag agg atg tgg
     694 950
     696 Trp Phe Met Ser Lys Gly Gly Thr Arg Ala Ser Ile Gln Arg Met Trp
     697     240                 245                 250
E--> 699 gat cct gtc gca tat gct ctt gga ttc att gac tgt gac aat atc agt
     700 998
     702 Asp Pro Val Ala Tyr Ala Leu Gly Phe Ile Asp Cys Asp Asn Ile Ser
     703 255                 260                 265                 270
E--> 705 gct cgg tgt atg ctc act ata ttt gca tta ttt gcc act aaa acg gag
     706 1046
     708 Ala Arg Cys Met Leu Thr Ile Phe Ala Leu Phe Ala Thr Lys Thr Glu
     709                 275                 280                 285
E--> 711 gct tcc cta tta cgc atg ctt aaa ggt tct ccg gac gtt tat ttg agt
     712 1094
     714 Ala Ser Leu Leu Arg Met Leu Lys Gly Ser Pro Asp Val Tyr Leu Ser
     715             290                 295                 300
E--> 717 ggt cca att aag aag tac atc ttg gat aag ggg gga agg ttt cac atg
     718 1142
     720 Gly Pro Ile Lys Lys Tyr Ile Leu Asp Lys Gly Gly Arg Phe His Met
     721         305                 310                 315
E--> 723 agg tgg ggg tgc aga cag gta ctc tat gag aca tcc tct gat ggc agt
     724 1190
     726 Arg Trp Gly Cys Arg Gln Val Leu Tyr Glu Thr Ser Ser Asp Gly Ser
     727     320                 325                 330
E--> 729 atg tat gtc agc ggg ctt gcc atg tca aag gcc act cag aag aaa gtt
     730 1238
     732 Met Tyr Val Ser Gly Leu Ala Met Ser Lys Ala Thr Gln Lys Lys Val
     733 335                 340                 345                 350
E--> 735 gta aaa gct gat gcc tat gtc gct gca tgt gat gtc cct gga att aaa
     736 1286
     738 Val Lys Ala Asp Ala Tyr Val Ala Ala Cys Asp Val Pro Gly Ile Lys
     739                 355                 360                 365
E--> 741 cga ttg gta cct cag aag tgg agg gaa ttg gaa ttc ttt gac aac att
     742 1334
     744 Arg Leu Val Pro Gln Lys Trp Arg Glu Leu Glu Phe Phe Asp Asn Ile
     745             370                 375                 380
```

same

RAW SEQUENCE LISTING DATE: 05/16/2001
PATENT APPLICATION: US/09/847,081 TIME: 15:06:10

Input Set : A:\DES.txt
Output Set: N:\CRF3\05162001\I847081.raw

```
E--> 747 tac aaa ttg gtt gga gtg cct gtt gtt acg gta caa cta cga tac aat
     748 1382
     750 Tyr Lys Leu Val Gly Val Pro Val Val Thr Val Gln Leu Arg Tyr Asn
     751         385                 390                 395
E--> 753 ggc tgg gtt aca gag ttg cag gac ttg gag cgt tcg agg caa ttg aag
     754 1430
     756 Gly Trp Val Thr Glu Leu Gln Asp Leu Glu Arg Ser Arg Gln Leu Lys
     757     400                 405                 410
E--> 759 cgc gct aca ggt ttg gac aat ctc ctg tat aca cca gat gca gat ttc
     760 1478
     762 Arg Ala Thr Gly Leu Asp Asn Leu Leu Tyr Thr Pro Asp Ala Asp Phe
     763 415                 420                 425                 430
E--> 765 tct tgc ttt gcg gac ctt gca ttg gca tct cct gaa gat tat tac att
     766 1526
     768 Ser Cys Phe Ala Asp Leu Ala Leu Ala Ser Pro Glu Asp Tyr Tyr Ile
     769                 435                 440                 445
E--> 771 gag ggc caa ggc tca ttg ctt caa tgt gtc ctt aca cct ggt gac cct
     772 1574
     774 Glu Gly Gln Gly Ser Leu Leu Gln Cys Val Leu Thr Pro Gly Asp Pro
     775             450                 455                 460
E--> 777 tac atg cct cta cta aat gat gaa atc ata aaa aga gtg tca aag cag
     778 1622
     780 Tyr Met Pro Leu Leu Asn Asp Glu Ile Ile Lys Arg Val Ser Lys Gln
     781         465                 470                 475
E--> 783 gtt ttg gca cta ttt cct tct tcc caa ggt ctt gag gtt acc tgg tca
     784 1670
     786 Val Leu Ala Leu Phe Pro Ser Ser Gln Gly Leu Glu Val Thr Trp Ser
     787     480                 485                 490
E--> 789 tca gtt gtg aaa att ggg caa tcc cta tat cgt gaa gga cct ggt aaa
     790 1718
     792 Ser Val Val Lys Ile Gly Gln Ser Leu Tyr Arg Glu Gly Pro Gly Lys
     793 495                 500                 505                 510
E--> 795 gac cca ttc aga cct gat cag aag act cca gtg gaa aat ttc ttt ctt
     796 1766
     798 Asp Pro Phe Arg Pro Asp Gln Lys Thr Pro Val Glu Asn Phe Phe Leu
     799                 515                 520                 525
E--> 801 gct ggc tca tat aca aaa cag gac tac ata gat agc atg gaa ggg gca
     802 1814
     804 Ala Gly Ser Tyr Thr Lys Gln Asp Tyr Ile Asp Ser Met Glu Gly Ala
     805             530                 535                 540
E--> 807 act ctt tca ggt agg caa gca tct gca tac gta tgt gat gct ggc gag
     808 1862
     810 Thr Leu Ser Gly Arg Gln Ala Ser Ala Tyr Val Cys Asp Ala Gly Glu
     811         545                 550                 555
E--> 813 aag ctg gtg gtg ttg cgg aaa aag att gct gct gct gag tca aac gag
     814 1910
     816 Lys Leu Val Val Leu Arg Lys Lys Ile Ala Ala Ala Glu Ser Asn Glu
     817     560                 565                 570
E--> 819 atc tct gaa ggt gta tca gta tct gat gag ttg agt ctt gtc tga
```

same

RAW SEQUENCE LISTING DATE: 05/16/2001
PATENT APPLICATION: US/09/847,081 TIME: 15:06:10

Input Set : A:\DES.txt
Output Set: N:\CRF3\05162001\I847081.raw

820 1955
822 Ile Ser Glu Gly Val Ser Val Ser Asp Glu Leu Ser Leu Val
823 575 580 585
E--> 825 tgactggaaa tcatccaatg aatactgaag agcacccccc actttgttaa tccgagaagc
826 2015
E--> 828 agatacaaac ataactcagt taggcattgc gtaaggaaga gttcttctaa attttgagtt
829 2075
E--> 831 cacaagatgg aaatcaaaag gttaaaatat gttgtatgta atattagtaa atcttcatag
832 2135
E--> 834 tgatgtatct attctgccac ccttcaggtt tagtgaaatg gatcgtattg ctcatcattc
835 2195
E--> 837 attgagaaga
838 2205
987 <210> SEQ ID NO: 10
988 <211> LENGTH: 23
989 <212> TYPE: DNA
990 <213> ORGANISM: Nicotiana tabacum
992 <400> SEQUENCE: 10
993 tacccgggct aaactacgct tgc 23
E--> 995 Le a 34 326
W--> 1000 Le A 34 326-Ausland
E--> 1003 - 17 -

done

delete at end of file

VERIFICATION SUMMARY DATE: 05/16/2001
PATENT APPLICATION: US/09/847,081 TIME: 15:06:12

Input Set : A:\DES.txt
Output Set: N:\CRF3\05162001\I847081.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:28 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:120 SEQ:1
M:254 Repeated in SeqNo=1
L:317 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:319 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:120 SEQ:3
M:254 Repeated in SeqNo=3
L:381 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:381 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:387 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:530 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
L:599 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:120 SEQ:5
M:254 Repeated in SeqNo=5
L:995 M:254 E: No. of Bases conflict, LENGTH:Input:326 Counted:26 SEQ:10
L:995 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:995 M:112 C: (48) String data converted to lower case,
L:1000 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
L:1003 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:1003 M:252 E: No. of Seq. differs, <211>LENGTH:Input:23 Found:26 SEQ:10